



PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/889,746

DATE: 02/08/2002
TIME: 11:18:39

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\02082002\1889746.raw

4 <110> APPLICANT: Ruelle, Jean-Louis
6 <120> TITLE OF INVENTION: Novel Compounds
9 <130> FILE REFERENCE: BM45352
11 <140> CURRENT APPLICATION NUMBER: 09/889,746
C--> 12 <141> CURRENT FILING DATE: 2001-12-31
14 <150> PRIOR APPLICATION NUMBER: 9901368.2
15 <151> PRIOR FILING DATE: 1999-01-22
17 <150> PRIOR APPLICATION NUMBER: 9901944.0
18 <151> PRIOR FILING DATE: 1999-01-28
20 <150> PRIOR APPLICATION NUMBER: 9902086.9
21 <151> PRIOR FILING DATE: 1999-01-29
23 <150> PRIOR APPLICATION NUMBER: 9903417.5
24 <151> PRIOR FILING DATE: 1999-02-15
26 <150> PRIOR APPLICATION NUMBER: 9903535.4
27 <151> PRIOR FILING DATE: 1999-02-16
29 <150> PRIOR APPLICATION NUMBER: PCT/EP00/00428
30 <151> PRIOR FILING DATE: 2000-01-19
32 <160> NUMBER OF SEQ ID NOS: 8
34 <170> SOFTWARE: FastSEQ for Windows Version 4.0
36 <210> SEQ ID NO: 1
37 <211> LENGTH: 1203
38 <212> TYPE: DNA
39 <213> ORGANISM: Neisseria meningitidis
41 <400> SEQUENCE: 1
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43 cagcagttgt acgctcaacc caatgagtca ttaccaacgg ttg
44 attaccatttg ataagagcgg tatggcactt gccaaatcgta tca
45 accaaaagttt tttatgaaga gcaaattcaa gagcaagcaa cag
46 gatgtatgg cacagctcat tccaaaggaa ggggtaagta gtg
47 gggcaaacca tgcacggcgtc tcaagtgc aa tttttgttaa atg
48 tcgcgagaca tctctagaca gcttaatagt atcaatccca atc
49 gtttatcag gagcaaccag tatttatggg tctggagcaa cag
50 gttactaagt ctgatttgg a agaggagcaa tttgaaaccc gca
51 aaatttatcca gtgaaggat cggttatcag gtaggtcaga gtg
52 aatggtaatg tccttgcacg acttgatgtc gactatcgca cca
53 gctaacggta aacgcacatcgc tcctgagcct gcccaaactg ata
54 ctaagtgtca atacaaatgt tgatggcaa cttgacgaca agc
55 ttgacgcatt ataacgcacaa acaagatacc gattatgcac ctg
56 gcggtgtgt ttggagaaaa gccttcattt aatgccatca aag
57 cagccaaaaaa ccacccaaag cacctttaat atcaactatc atc
58 aacaccatca ataccaatgc ttattatcgc agagagaaa gca
59 gccccgtttt cgatcgccaa agccctgcct attttacaaa gca
60 acttttgatg cttataccaa ggctccacaa gctcgcgcct atg

ENTERED

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61 tctaaggcag aggtactagg gcgtgtccct aatttgaata agcccaaaag agccctattt 1200
62 taa 1203
64 <210> SEQ ID NO: 2
65 <211> LENGTH: 400
66 <212> TYPE: PRT
67 <213> ORGANISM: Neisseria meningitidis
69 <400> SEQUENCE: 2
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71 1 5 10 15
72 Val Ala Val Thr Gln Gln Leu Tyr Ala Gln Pro Asn Glu Ser Leu Pro
73 20 25 30
74 Thr Val Glu Leu Glu Pro Val Val Ile Thr Ile Asp Lys Ser Gly Met
75 35 40 45
76 Ala Leu Ala Asn Arg Ile Thr Gln Met Pro His Thr Thr Lys Val Ile
77 50 55 60
78 Tyr Glu Glu Gln Ile Gln Glu Gln Ala Thr Gly Ser Arg Gln Leu Ala
79 65 70 75 80
80 Asp Val Met Ala Gln Leu Ile Pro Ser Leu Gly Val Ser Ser Gly Thr
81 85 90 95
82 Thr Ser Asn Phe Gly Gln Thr Met His Gly Arg Gln Val Gln Phe Leu
83 100 105 110
84 Leu Asn Gly Val Pro Leu Thr Gly Ser Arg Asp Ile Ser Arg Gln Leu
85 115 120 125
86 Asn Ser Ile Asn Pro Asn Gln Val Ala Arg Ile Glu Val Leu Ser Gly
87 130 135 140
88 Ala Thr Ser Ile Tyr Gly Ser Gly Ala Thr Gly Gly Leu Ile Asn Ile
89 145 150 155 160
90 Val Thr Lys Ser Asp Leu Glu Glu Gln Phe Glu Thr Arg Ile Gly
91 165 170 175
92 Val His Gly Ser Lys Leu Ser Ser Glu Gly Ile Gly Tyr Gln Val Gly
93 180 185 190
94 Gln Ser Val Ala Gly Val Ser Glu Asn Gly Asn Val Leu Ala Arg Leu
95 195 200 205
96 Asp Val Asp Tyr Arg Thr Thr Gly Gly Ala Phe Asp Ala Asn Gly Lys
97 210 215 220
98 Arg Ile Ala Pro Glu Pro Ala Gln Thr Asp Lys Gln Asp Ser Lys Ser
99 225 230 235 240
100 Leu Ser Val Asn Thr Asn Val Asp Trp Gln Leu Asp Asp Lys Gln Asn
101 245 250 255
102 Ile Asn Leu Ala Leu Thr His Tyr Asn Asp Lys Gln Asp Thr Asp Tyr
103 260 265 270
104 Ala Pro Asp Tyr Gly Asn Arg Leu Ala Val Leu Phe Gly Glu Lys Pro
105 275 280 285
106 Ser Leu Asn Ala Ile Lys Gly Leu Ser Leu Ser Glu Gln Pro Lys Thr
107 290 295 300
108 Thr Lys Ser Thr Phe Asn Ile Asn Tyr His His Asp Asp Leu Trp Gly
109 305 310 315 320
110 Asn Thr Ile Asn Thr Asn Ala Tyr Tyr Arg Arg Glu Lys Gly Arg Phe
111 325 330 335

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112 Tyr Pro Phe Val Ala Pro Phe Ser Ile Ala Lys Ala Leu Pro Ile Leu
113 340 345 350
114 Gln Ser Met Asn Leu Pro Ser Ala Thr Leu Asp Ala Tyr Thr Lys Ala
115 355 360 365
116 Pro Gln Ala Arg Ala Tyr Gly Val Leu Gln Ser Glu Ser Lys Ala Glu
117 370 375 380
118 Val Leu Gly Arg Val Pro Asn Leu Asn Lys Pro Lys Arg Ala Leu Phe
119 385 390 395 400
121 <210> SEQ ID NO: 3
122 <211> LENGTH: 2409
123 <212> TYPE: DNA
124 <213> ORGANISM: Neisseria meningitidis
126 <400> SEQUENCE: 3
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128 cattgcggc cgcgcgatgc cggtgcggcg gagaaaaacgg acaatccgac cgccggagga 120
129 agtgttcgga gcgtgtccga acccatgcag cctgcccggc tgagcctcggtt tcgacacctgc 180
130 ctgttttgcgtt gtaacgaaag cggcaaaaccc gaaaaaaacgg aatctgcgtt caaaggaagc 240
131 ggcgaagggc ctgtgcccga aaaccacacg cgaattgtcg cgcacaagggt ggaaggcggcag 300
132 tcgcaggtca aggtacgcgc ggaggggcggc gtcgttgcgtt aacgcacccg gacgaccctt 360
133 aatgcgcact gggcggatta cgaccagtcg ggcgacacccg ttaccgtagg cgaccgggttc 420
134 gcccctcaac aggacgggtac gtcgttgcgtt ggcgaaaccc tgacctacaa tctcgagcag 480
135 cagaccggcg aagcgcacaa cgtccgcacatg gaaaccgaaac aaggcggacg gcggctgcac 540
136 agcgtcggcc gcaccgcga aatgttggc gaagggcatt acaaaactgac ggaacccaa 600
137 ttcaacaccc ttccgcggc cgatgcgcgc tggatgtca aggcagcctc tgcgttgcgtt 660
138 gatcgaaagaa aaggcatagg cgttgcacaa cacgcgcct tcgtgttgcgtt cggcggttcc 720
139 attttctaca ccccttggc ggacttcccg cttgacggca accgcacaaag cggcctgcctt 780
140 gttccctcac tgcgttgcgtt ttcggacggc gtttccctt ccgttcccta ttatccaaac 840
141 cttgcgcgcgc atctcgatgc cacgttgcgc cccagcgtga tcggcgaacg cgccgggttc 900
142 tttgacggggc aggtacgcata cctgcggccg gattatgcgc gccagtcgc cctgacctgg 960
143 ctgcgcacg acaagaaaaag cggcaggaat aacgcgtatc aggcgaaatg gcagcatcg 1020
144 cacgacattt ccgcacacgc tcaggcgggt gtcgatttca accaagtctc cgacagcggc 1080
145 tactaccgcg acttttacgg caacaaagaa atcgcgcgc acgtcaaccc caaccgcgtt 1140
146 gtatggctgg attatggcgg cagggcggcg ggcggcagcc tgaatgcgcgc ctttcgggtt 1200
147 ctgaaataacc agacgctggc aaacccaaacg ggctacaaag acaaaacccgtt tgcctgtatg 1260
148 cccgcgcctt ccgcgcattt ggcgcacaaac accggcaggc cgccaaatcgg cgtgtccgc 1320
149 caatttaccc gcttcagccca cgacagccgc caagacggca gccgcctcggtt cgtctatccc 1380
150 gacatcaaat gggatttcag caacagctgg gttacgtcc gtcccaaact cgactgcac 1440
151 gcccacattt acagcctcaa ccgcgttgcgc agccaaagaa cccgcgcgtt cagccgcact 1500
152 ctacccatcg tcaacatcgca cagcggcatg accttcgaaac gcaatacgcg gatgttgcgc 1560
153 ggagaagtcc tgcacaaacccct cgagccgcgc ctgttctaca actatattcc tgcacaaatcc 1620
154 caaaaacgacc tgcacaaatcc ttgattcgtcg gaaagcagct tcggctacgg gcagcttttt 1680
155 cgtaaaaacc tctattacgg caacgcacagg attaacacccg caaaacgcctt ttccgcgc 1740
156 gtgcaaaagcc gtatccggc cggcgcgcac ggggcagac gtttccgcgc cgccatcg 1800
157 cagaaattct acttcaaaaaa cgacgcagtc atgcttgcgtt gcagtgtcg gaaaaaaacgg 1860
158 cgcagccgtt ccgcactgggt ggcattcgcgc tccagcggca tcggcagccg ctttccatcctc 1920
159 gacagcagca tccactacaa cccaaacgcac aaacgcgcgc agaactacgc cgtcgggtgc 1980
160 agctaccgtc ccgcacacaggc caaagtgcgtt aacgcggcgtt acaaaatacg ggcacacgaa 2040
161 aaaaatctacc tgaagtcgtt cgggttccat ttttacgaca aactcagccca gctcgacctg 2100
162 tccgcacaat ggccctgac ggcacccgtt tcggccgtcg tccgttacaa ctacgggtttt 2160

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163	gaagccaaaa aaccgataga ggtgctggcg ggtgcggaat acaaaaagcag ttgcggctgc	2220
164	tggggcgcgg gcgtgtacgc ccaacgctac gttaccggcg aaaaacaccta caaaaacgct	2280
165	gtctttttct cacttcagtt gaaagaccc tc agcagtgtcg gcagaaaaccc cgcagacagg	2340
166	atggatgtcg ccgttcccggtatccccc gcccactctc tttccgcgg acgcaacaaa	2400
167	cggccctga	2409
169	<210> SEQ ID NO: 4	
170	<211> LENGTH: 802	
171	<212> TYPE: PRT	
172	<213> ORGANISM: Neisseria meningitidis	
174	<400> SEQUENCE: 4	
175	Met Ala Arg Leu Phe Ser Leu Lys Pro Leu Val Leu Ala Leu Gly Phe	
176	1 5 10 15	
177	Cys Phe Gly Thr His Cys Ala Ala Ala Asp Ala Val Ala Ala Glu Glu	
178	20 25 30	
179	Thr Asp Asn Pro Thr Ala Gly Gly Ser Val Arg Ser Val Ser Glu Pro	
180	35 40 45	
181	Met Gln Pro Ala Gly Leu Ser Leu Gly Ser Thr Cys Leu Phe Cys Ser	
182	50 55 60	
183	Asn Glu Ser Gly Lys Pro Glu Lys Thr Glu Ser Ala Val Lys Gly Ser	
184	65 70 75 80	
185	Gly Glu Gly Pro Val Pro Glu Asn His Thr Arg Ile Val Ala Asp Lys	
186	85 90 95	
187	Val Glu Gly Gln Ser Gln Val Lys Val Arg Ala Glu Gly Gly Val Val	
188	100 105 110	
189	Val Glu Arg Asn Arg Thr Thr Leu Asn Ala Asp Trp Ala Asp Tyr Asp	
190	115 120 125	
191	Gln Ser Gly Asp Thr Val Thr Val Gly Asp Arg Phe Ala Leu Gln Gln	
192	130 135 140	
193	Asp Gly Thr Leu Ile Arg Gly Glu Thr Leu Thr Tyr Asn Leu Glu Gln	
194	145 150 155 160	
195	Gln Thr Gly Glu Ala His Asn Val Arg Met Glu Thr Glu Gln Gly Gly	
196	165 170 175	
197	Arg Arg Leu Gln Ser Val Ser Arg Thr Ala Glu Met Leu Gly Glu Gly	
198	180 185 190	
199	His Tyr Lys Leu Thr Glu Thr Gln Phe Asn Thr Cys Ser Ala Gly Asp	
200	195 200 205	
201	Ala Gly Trp Tyr Val Lys Ala Ala Ser Val Glu Ala Asp Arg Glu Lys	
202	210 215 220	
203	Gly Ile Gly Val Ala Lys His Ala Ala Phe Val Phe Gly Gly Val Pro	
204	225 230 235 240	
205	Ile Phe Tyr Thr Pro Trp Ala Asp Phe Pro Leu Asp Gly Asn Arg Lys	
206	245 250 255	
207	Ser Gly Leu Leu Val Pro Ser Leu Ser Ala Gly Ser Asp Gly Val Ser	
208	260 265 270	
209	Leu Ser Val Pro Tyr Tyr Phe Asn Leu Ala Pro Asn Leu Asp Ala Thr	
210	275 280 285	
211	Phe Ala Pro Ser Val Ile Gly Glu Arg Gly Ala Val Phe Asp Gly Gln	
212	290 295 300	
213	Val Arg Tyr Leu Arg Pro Asp Tyr Ala Gly Gln Ser Asp Leu Thr Trp	

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214	305	310	315	320
215	Leu Pro His Asp Lys Lys Ser Gly Arg Asn Asn Arg Tyr Gln Ala Lys			
216	325	330	335	
217	Trp Gln His Arg His Asp Ile Ser Asp Thr Leu Gln Ala Gly Val Asp			
218	340	345	350	
219	Phe Asn Gln Val Ser Asp Ser Gly Tyr Tyr Arg Asp Phe Tyr Gly Asn			
220	355	360	365	
221	Lys Glu Ile Ala Gly Asn Val Asn Leu Asn Arg Arg Val Trp Leu Asp			
222	370	375	380	
223	Tyr Gly Gly Arg Ala Ala Gly Gly Ser Leu Asn Ala Gly Leu Ser Val			
224	385	390	395	400
225	Leu Lys Tyr Gln Thr Leu Ala Asn Gln Ser Gly Tyr Lys Asp Lys Pro			
226	405	410	415	
227	Tyr Ala Leu Met Pro Arg Leu Ser Ala Asp Trp Arg Lys Asn Thr Gly			
228	420	425	430	
229	Arg Ala Gln Ile Gly Val Ser Ala Gln Phe Thr Arg Phe Ser His Asp			
230	435	440	445	
231	Ser Arg Gln Asp Gly Ser Arg Leu Val Val Tyr Pro Asp Ile Lys Trp			
232	450	455	460	
233	Asp Phe Ser Asn Ser Trp Gly Tyr Val Arg Pro Lys Leu Gly Leu His			
234	465	470	475	480
235	Ala Thr Tyr Tyr Ser Leu Asn Arg Phe Gly Ser Gln Glu Ala Arg Arg			
236	485	490	495	
237	Val Ser Arg Thr Leu Pro Ile Val Asn Ile Asp Ser Gly Met Thr Phe			
238	500	505	510	
239	Glu Arg Asn Thr Arg Met Phe Gly Gly Glu Val Leu Gln Thr Leu Glu			
240	515	520	525	
241	Pro Arg Leu Phe Tyr Asn Tyr Ile Pro Ala Lys Ser Gln Asn Asp Leu			
242	530	535	540	
243	Pro Asn Phe Asp Ser Ser Glu Ser Ser Phe Gly Tyr Gly Gln Leu Phe			
244	545	550	555	560
245	Arg Glu Asn Leu Tyr Tyr Gly Asn Asp Arg Ile Asn Thr Ala Asn Ser			
246	565	570	575	
247	Leu Ser Ala Ala Val Gln Ser Arg Ile Leu Asp Gly Ala Thr Gly Ala			
248	580	585	590	
249	Glu Arg Phe Arg Ala Gly Ile Gly Gln Lys Phe Tyr Phe Lys Asn Asp			
250	595	600	605	
251	Ala Val Met Leu Asp Gly Ser Val Gly Lys Lys Pro Arg Ser Arg Ser			
252	610	615	620	
253	Asp Trp Val Ala Phe Ala Ser Ser Gly Ile Gly Ser Arg Phe Ile Leu			
254	625	630	635	640
255	Asp Ser Ser Ile His Tyr Asn Gln Asn Asp Lys Arg Ala Glu Asn Tyr			
256	645	650	655	
257	Ala Val Gly Ala Ser Tyr Arg Pro Ala Gln Gly Lys Val Leu Asn Ala			
258	660	665	670	
259	Arg Tyr Lys Tyr Gly Arg Asn Glu Lys Ile Tyr Leu Lys Ser Asp Gly			
260	675	680	685	
261	Ser Tyr Phe Tyr Asp Lys Leu Ser Gln Leu Asp Leu Ser Ala Gln Trp			
262	690	695	700	

VERIFICATION SUMMARY
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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date